

6660843

## FIG. 1

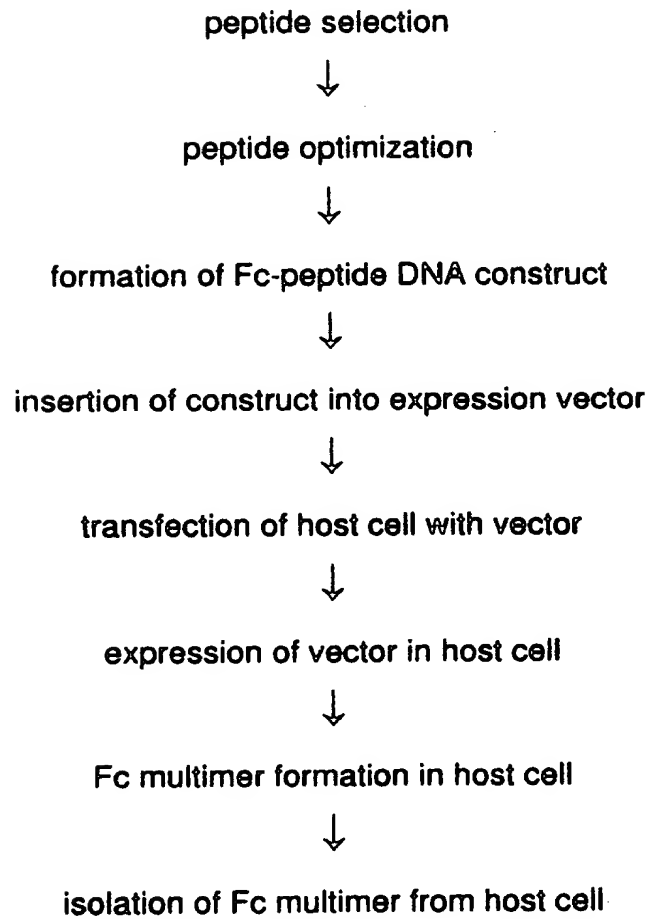


FIG. 2A

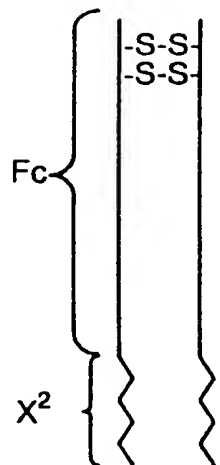


FIG. 2B

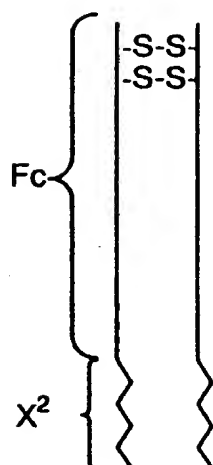


FIG. 2C

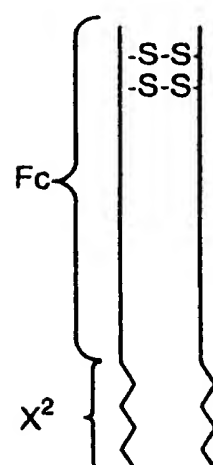


FIG. 2D

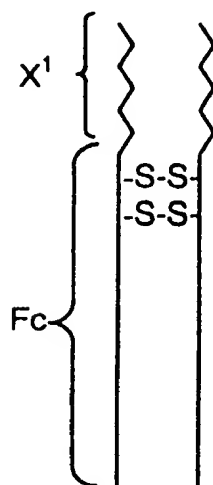


FIG. 2E

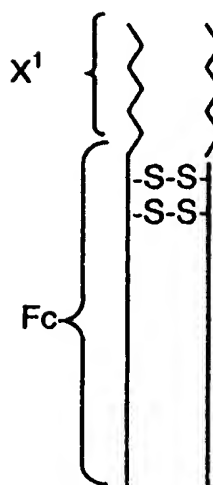


FIG. 2F

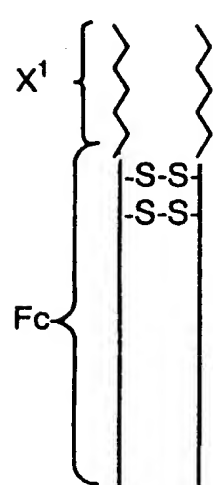


FIG. 3A

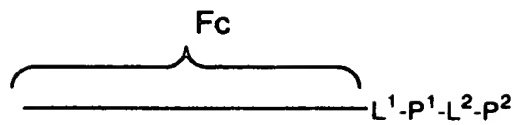


FIG. 3B

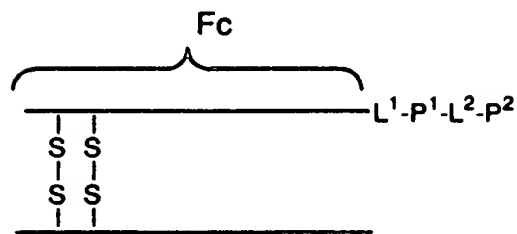
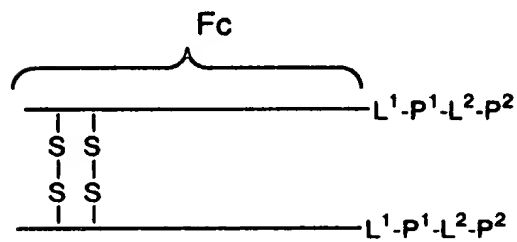


FIG. 3C



# FIG. 4

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ATGGACAAAAC TCACACATGTCCACCTTGTCCAGCTCCGGAAC TCCTGGGGGGACCGTCA
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCGTTCGCGGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K -

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

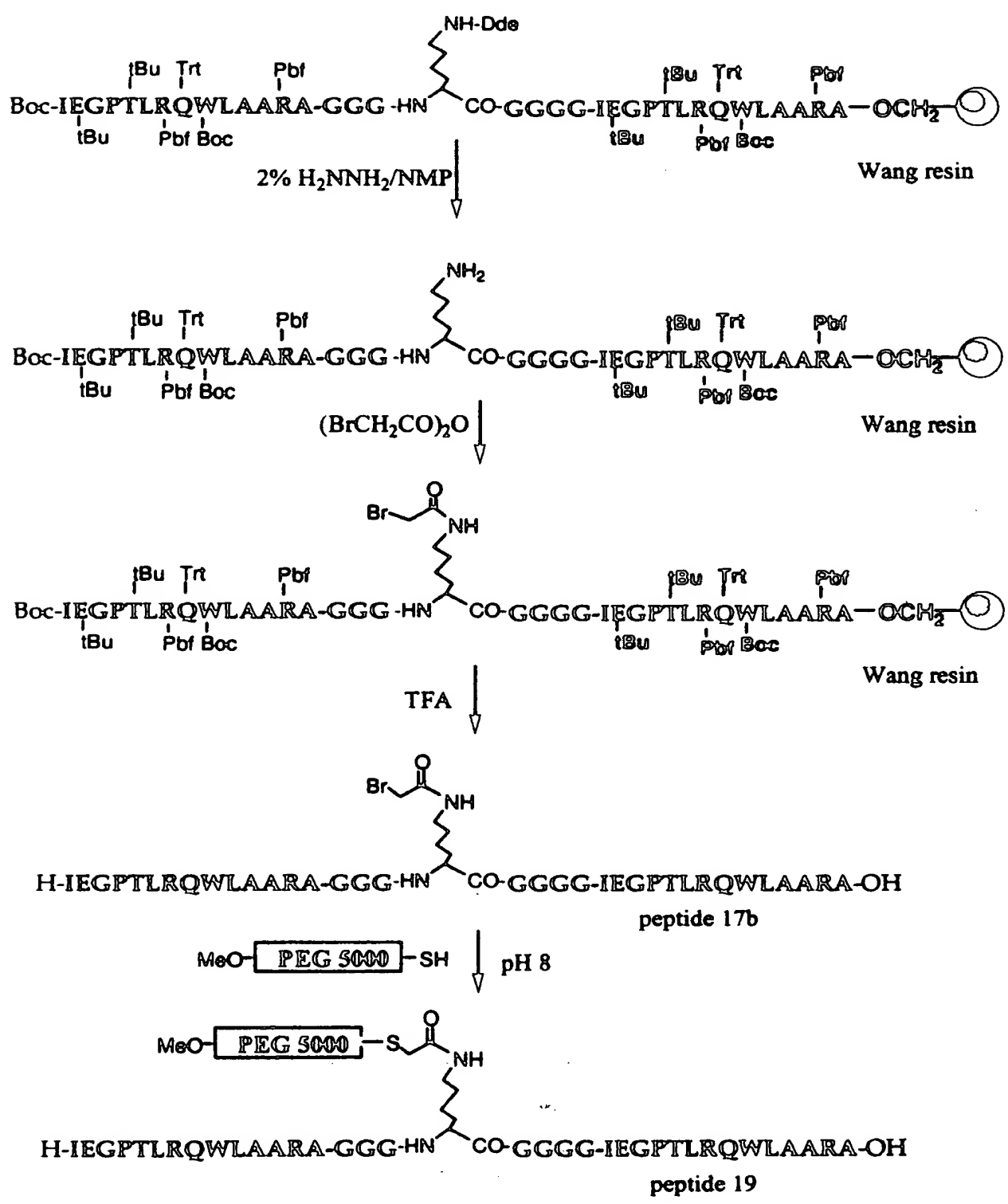


FIG. 6

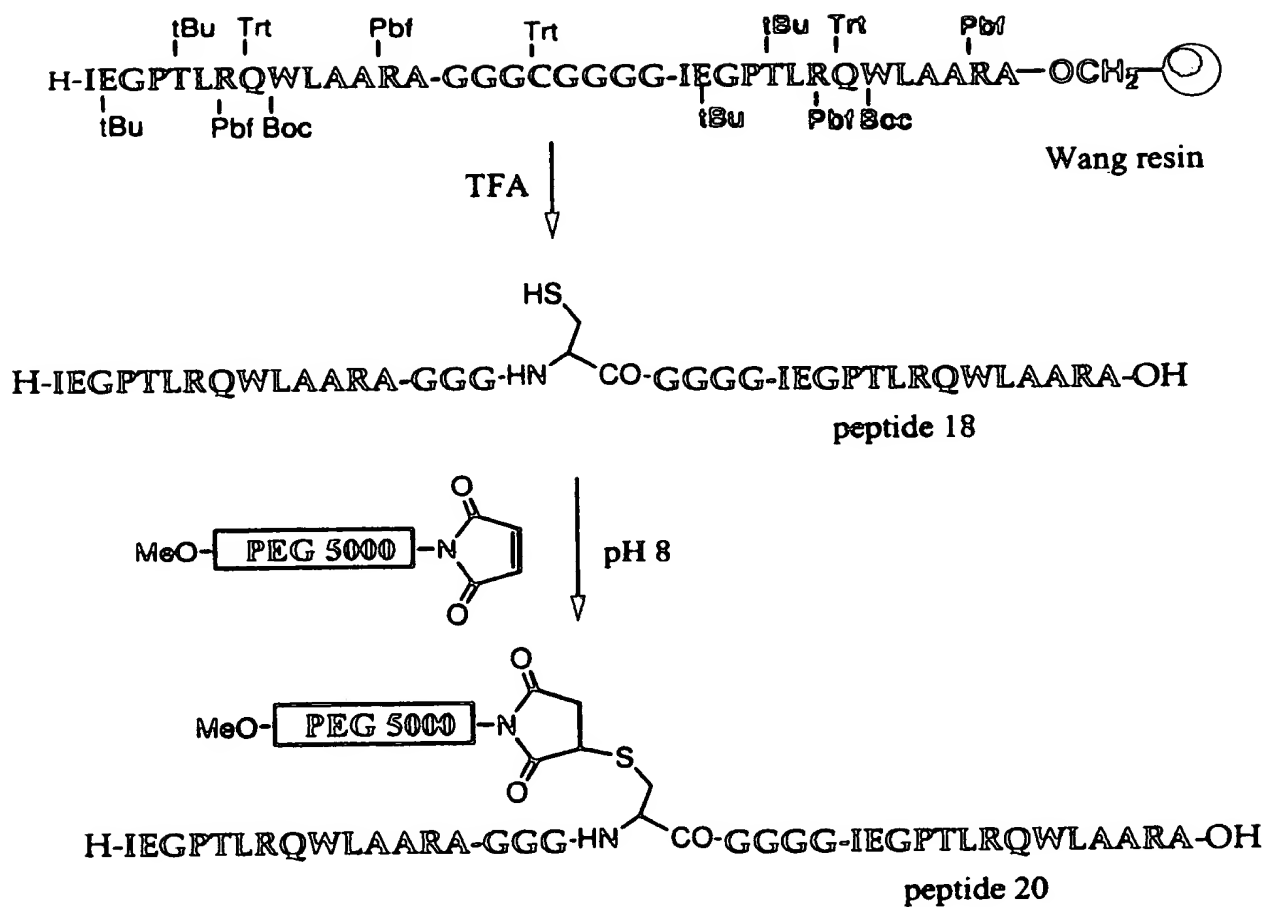


FIG. 7

XbaI  
 |  
 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC  
 1 .....+.....+.....+.....+.....+ 60  
 AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTGGAGTGTGTACAG  
 C M D K T H T C P -  
 CACCTTGTCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC  
 61 .....+.....+.....+.....+.....+ 120  
 GTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG  
 C P C P A P E L L G G P S V F L F P P K P -  
 CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGGACGTGA  
 121 .....+.....+.....+.....+.....+ 180  
 GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT  
 C K D T L M I S R T P E V T C V V V D V S -  
 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG  
 181 .....+.....+.....+.....+.....+ 240  
 CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC  
 C H E D P E V K F N W Y V D G V E V H N A -  
 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA  
 241 .....+.....+.....+.....+.....+ 300  
 GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCGTGCATGGCACACCAGTCCGAGGAGT  
 C K T K P R E E Q Y N S T Y R V V S V L T -  
 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG  
 301 .....+.....+.....+.....+.....+ 360  
 GGCAGGACGTGGTCTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTTGTTTC  
 C V L H Q D W L N G K E Y K C K V S N K A -  
 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC  
 361 .....+.....+.....+.....+.....+ 420  
 GGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTTTCGGTTTCCCGTCGGGGCTCTTGGTG  
 C L P A P I E K T I S K A K G Q P R E P Q -  
 AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT  
 421 .....+.....+.....+.....+.....+ 480  
 TCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCCGACTGGA  
 C V Y T L P P S R D E L T K N Q V S L T C -  
 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC  
 481 .....+.....+.....+.....+.....+ 540  
 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
 C L V K G F Y P S D I A V E W E S N G Q P -  
 CGGAGAACAACCTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT  
 541 .....+.....+.....+.....+.....+ 600  
 GCCTCTTGTGTTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA  
 C E N N Y K T T P P V L D S D G S F F L Y -  
 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG  
 601 .....+.....+.....+.....+.....+ 660  
 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC  
 C S K L T V D K S R W Q Q G N V F S C S V -  
 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA  
 661 .....+.....+.....+.....+.....+ 720  
 ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT  
 C M H E A L H N H Y T Q K S L S L S P G K -  
 AAGGTGGAGGTGGTGGTATCGAAGGTCCGACTCTGCGTCAGTGGCTGGCTGCTCGTGCTT  
 721 .....+.....+.....+.....+.....+ 780  
 TTCCACCTCCACCACCATAGCTTCCAGGCTGAGACGCAGTCACCGACCGACGAGCACGAA  
 C G G G G G I E G P T L R Q W L A A R A \* -  
 BamHI  
 |  
 AATCTCGAGGATCC  
 781 .....+..... 794  
 TTAGAGCTCCTAGG

A ☆ -



841 GTAAATAATGGATCC 855  
-----+-----  
CATTATTACCTAGG  
K \*

FIG. 10

FIG. 10

XbaI  
|  
TCTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
AGATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG  
M I E G P T L R -

GTCAGTGGCTGGCTGCTCGTGCTGGTGGAGGCCGTGGGGACAAAACTCACACATGTCCAC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
CAGTCACCGACCGACGAGCAGCACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG  
Q W L A A R A G G G G G D K T H T C P P -

CTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
GAACGGGTCTGTTGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGCGGGGTTTTGGGT  
C P A P E L L G G P S V F L F P P K P K -

AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACCTCGG  
D T L M I S R T P E V T C V V V D V S H -

ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT  
E D P E V K F N W Y V D G V E V H N A K -

AGACAAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACAGTCCGAGGAGTGGC  
T K P R E E Q Y N S T Y R V V S V L T V -

TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
AGGACGTGGTCTTGACCGACTTACCGTTCTCATGTTTACGTTCCAGAGGTTGTTTCGGG  
L H Q D W L N G K E Y K C K V S N K A L -

TCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
AGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCGCTCGGGGCTCTTGGTGTCC  
P A P I E K T I S K A K G Q P R E P Q V -

TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
ACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGG  
Y T L P P S R D E L T K N Q V S L T C L -

TGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC  
V K G F Y P S D I A V E W E S N G Q P E -

AGAACAACACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660  
TCTTGTGTGATGTTCTGGTCCGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGATGT  
N N Y K T T P P V L D S D G S F F L Y S -

GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720  
CGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT  
K L T V D K S R W Q Q G N V F S C S V M -

TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
ACGTACTIONGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCCATTTA  
H E A L H N H Y T Q K S L S L S P G K \* -

BamHI  
|  
AATGGATCC  
----- 789  
TTACCTAGG

FIG.11

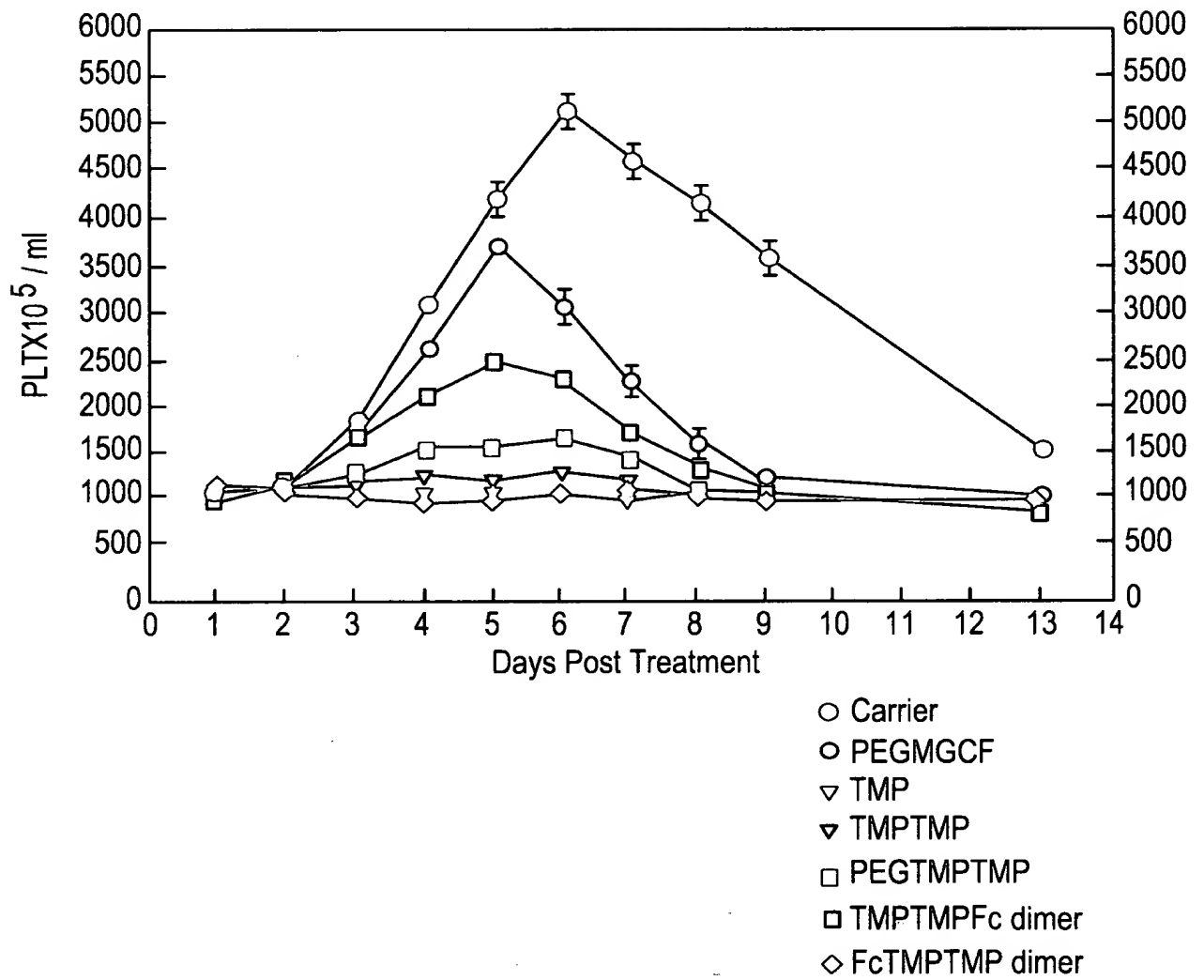


FIG.12

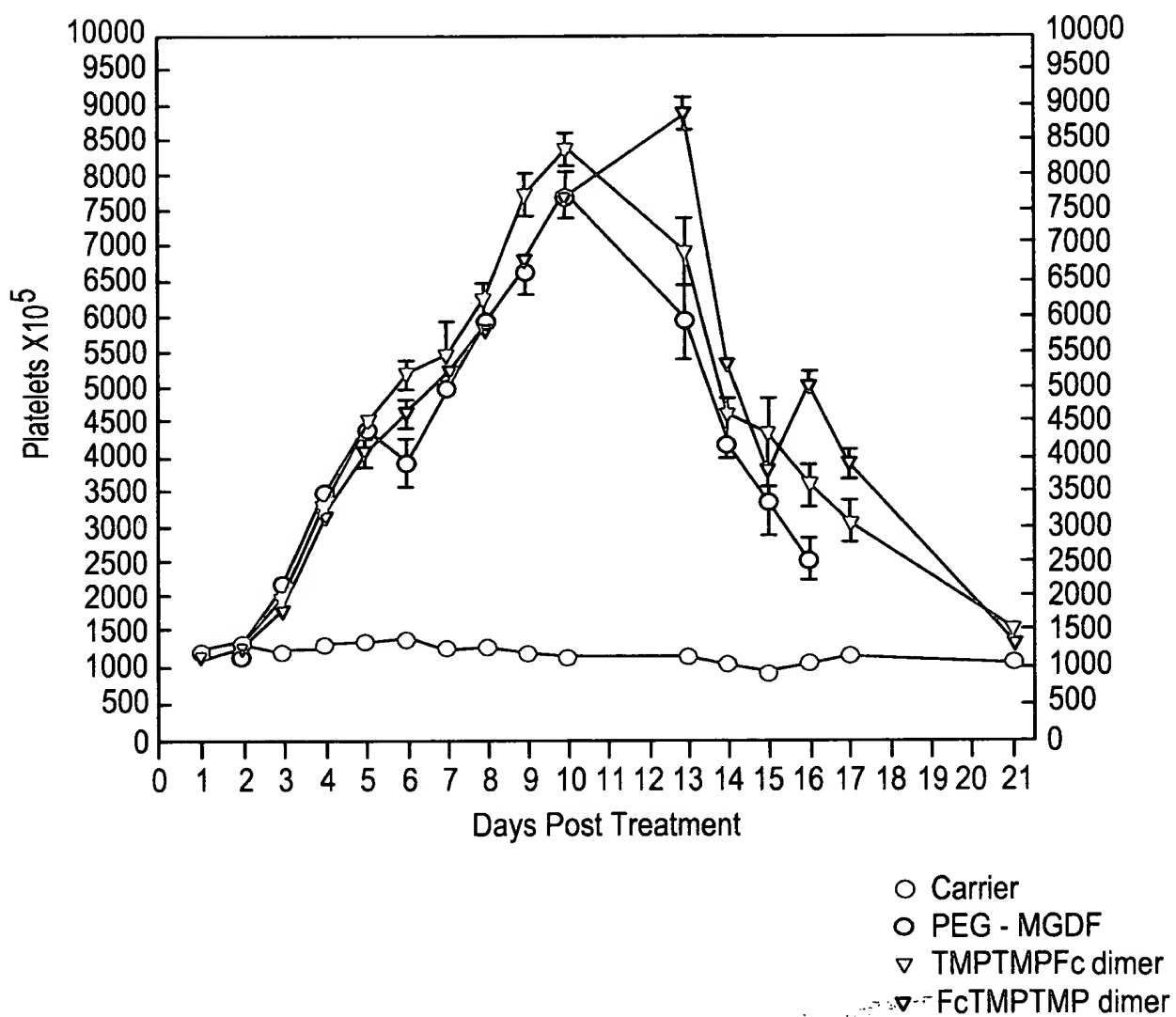


FIG. 13

XbaI

TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACCTCACACATGTC  
 1 AGATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG 60  
 CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC  
 51 GTGGAACAGGTCGAGGCCCTTGGAGCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTTTG 120  
 P C P A P E L L G G P S V F L F P P K P  
 CCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA  
 21 GGTTCTCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTGTACGCCACCACCACCTGCACT 180  
 K D T L M I S R T P E V T C V V V D V S  
 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG  
 31 CGGTGCTTCTGGGACTCCAGTTCAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC 240  
 H E D P E V K F N W Y V D G V E V H N A  
 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA  
 41 GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT 300  
 K T K P R E E Q Y N S T Y R V V S V L T  
 CCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG  
 51 GGCAGGACGTGGTCTGACCGACTTACCGTTTCTCATGTTTACGTTCCAGAGGTTGTTTC 360  
 V L H Q D W L N G K E Y K C K V S N K A  
 CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC  
 61 GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420  
 L P A P I E K T I S K A K G Q P R E P Q  
 AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCCTGACCT  
 71 TCCACATGTGGGACGGGGTAGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA 480  
 V Y T L P P S R D E L T K N Q V S L T C  
 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC  
 81 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG 540  
 L V K G F Y P S D I A V E W E S N G Q P  
 CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCT  
 91 GCCTCTTGTGATGTTCTGGTGGGAGGGCAGCACCTGAGGCTGCCGAGGAAGAAGGAGA 600  
 E N N Y K T T P P V L D S D G S F F L Y  
 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG  
 101 TGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGAGAAGAGTACGAGGC 660  
 S K L T V D K S R W Q Q G N V F S C S V  
 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA  
 111 ACTACGTA TCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT 720  
 M H E A L H N H Y T Q K S L S L S P G K  
 AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCCGCTGACTTGGGTTT  
 121 TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGGCAGTGAACCCAAA 780  
 G G G G G G G T Y S C H F G P L T W V C

**BamHI**

781 GCAAACCGCAGGGTGGTTAATCTCGTGGATCC 812  
 .....+.....+.....+.....  
 CGTTTGCGCTCCCAACCAATTAGAGCACCTAGG  
 K P O G G \*

FIG. 14

XbaI  
|  
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC 60  
-----+-----+-----+-----+-----+  
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCCTCCATGAATGAGAACGG  
c M G G T Y S C H -

61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGACA 120  
-----+-----+-----+-----+-----+  
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCCACCCCTCCGCCCCCTGT  
c F G P L T W V C K P Q G G G G G G G D K -

121 AAATCACACATGTCCACCTTGCCAGCACCTGAACCTCTGGGGGACCGTCAGTTTTTC 180  
-----+-----+-----+-----+-----+  
TTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCTCCGAGTCAAAAGG  
c T H T C P P C P A P E L L G G P S V F L -

181 TCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTACATGCG 240  
-----+-----+-----+-----+-----+  
AGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGG  
c F P P K P K D T L M I S R T P E V T C V -

241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300  
-----+-----+-----+-----+-----+  
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGC  
c V V D V S H E D P E V K F N W Y V D G V -

301 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG 360  
-----+-----+-----+-----+-----+  
ACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCAC  
c E V H N A K T K P R E E Q Y N S T Y R V -

361 TGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA 420  
-----+-----+-----+-----+-----+  
ACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCTCATGTTACGT  
c V S V L T V L H Q D W L N G K E Y K C K -

421 AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGC 480  
-----+-----+-----+-----+-----+  
TCCAGAGGTTGTTTCGGGAGGGTTCGGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCCG  
c V S N K A L P A P I E K T I S K A K G Q -

481 AGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC 540  
-----+-----+-----+-----+-----+  
TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTCTTGG  
c P R E P Q V Y T L P P S R D E L T K N Q -

541 AGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG 600  
-----+-----+-----+-----+-----+  
TCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC  
c V S L T C L V K G F Y P S D I A V E W E -

601 AGAGCAATGGGCAGCCGAGAACAATAACAAGACCACGCCTCCCGTGCTGGACTCCGACG 660  
-----+-----+-----+-----+-----+  
TCTCGTTACCCGTCCGCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGC  
c S N G Q P E N N Y K T T P P V L D S D G -

661 GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG 720  
-----+-----+-----+-----+-----+  
CGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGC  
c S F F L Y S K L T V D K S R W Q Q G N V -

721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780  
-----+-----+-----+-----+-----+  
AGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGA  
c F S C S V M H E A L H N H Y T Q K S L S -

BamHI  
|  
781 CCCTGTCTCCGGGTAAATAATGGATCC 807  
-----+-----+-----+-----+-----+  
GGGACAGAGGCCCATTTATTACCTAGG  
c L S P G K \*

FIG. 15

XbaI

TCTAGATTTGAGTTTAACTTTTAGAAGGAGGAATAAAAATATGGAGGTACTTACTCTTG  
-----+-----+-----+-----+-----+-----+-----+-----+ 60  
AGATCTAAACTCAA AATTGAAAATCTTCCTCCTTATTTTATACCCCTCCATGAATGAGAAC  
M G G T Y S C -  
  
CCACTTCGGCCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCCGGCGCGCGGTGG  
-----+-----+-----+-----+-----+-----+-----+-----+ 120  
GGTGAAGCCGGGTGACTGAACCCAACGTTTGGCGTCCCACC GCCCGCCGCCGCCACCC  
H F G P L T W V C K P Q G G G G G G G G -  
  
TACCTATTCTGTCA TTTTGGCCCCGCTGACCTGGGTATGTAAGCCACAAGGGGGTGGGGG  
-----+-----+-----+-----+-----+-----+-----+-----+ 180  
ATGGATAAGGACAGTAA AACCGGGCGACTGGACCCATACATTCCGTGTTCCCCCACCCCC  
T Y S C H F G P L T W V C K P Q G G G G G -  
  
AGGCGGGGGGGACAAA ACTCACACATGTCCACCTTGCCAGCACCTGAACTCCTGGGGGG  
-----+-----+-----+-----+-----+-----+-----+-----+ 240  
TCCGCCCCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCC  
G G G D K T H T C P P C P A P E L L G G -  
  
ACCGTCAGTTTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC  
-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGG  
P S V F L F P P K P K D T L M I S R T P -  
  
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTG  
-----+-----+-----+-----+-----+-----+-----+-----+ 360  
ACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC  
E V T C V V V D V S H E D P E V K F N W -  
  
GTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA  
-----+-----+-----+-----+-----+-----+-----+-----+ 420  
CATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCA GTT  
Y V D G V E V H N A K T K P R E E Q Y N -  
  
CAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAA  
-----+-----+-----+-----+-----+-----+-----+-----+ 480  
GTCGTGCATGGCACACCA GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTT  
S T Y R V V S V L T V L H Q D W L N G K -  
  
GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC  
-----+-----+-----+-----+-----+-----+-----+-----+ 540  
CCTCATGTTACGTTTCCAGAGGTTGTTTCGGGAGGGTCGGGGTAGCTCTTTTGGTAGAG  
E Y K C K V S N K A L P A P I E K T I S -  
  
CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGA  
-----+-----+-----+-----+-----+-----+-----+-----+ 600  
GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACT  
K A K G Q P R E P Q V Y T L P P S R D E -  
  
GCTGACCAAGAACCAGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT  
-----+-----+-----+-----+-----+-----+-----+-----+ 660  
CGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCA GTTTCGAAGATAGGGTCGCTGTA  
L T K N Q V S L T C L V K G F Y P S D I -  
  
CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACA ACTACAAGACCACGCCTCCCCGT  
-----+-----+-----+-----+-----+-----+-----+-----+ 720  
GCGGCACCTCACCCCTCTCGTTACCCGTCGGCCCTCTTGTTGATGTTCTGGTGGGAGGGCA  
A V E W E S N G Q P E N N Y K T T P P V -  
  
GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG  
-----+-----+-----+-----+-----+-----+-----+-----+ 780  
CGACCTGAGGCTCGCCGAGGAAGAAGGAGATGTCGTT CGAGTGCCACCTGTTCTCGTCCAC  
L D S D G S F F L Y S K L T V D K S R W -  
  
GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC  
-----+-----+-----+-----+-----+-----+-----+-----+ 840  
CGTCGTCCCTTTCGAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTATGT  
O O G N V F S C S V M H E A L H N H Y T -

**BamHI**

GCAGAAGAGCCTCTCCCTGTCTCCGGTAAATAATGGATCC  
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 881  
CGTCTTCTCGGAGAGGGACAGAGGCCCAATTATTACCTAGG  
O K S L S L S P G K \*

# FIG. 16

XbaI

1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60

AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG

M D K T H T C P

61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAAC 120

GTGGAACGGTCTGTGGACTTGAGGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTTG

P C P A P E L L G G P S V F L F P P K P

121 CCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180

GGTTCCTGTGGGAGTACTAGAGGGCCTGGGACTCCAGTGTACGCACCAACCTGCACCT

K D T L M I S R T P E V T C V V V D V S

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240

CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC

H E D P E V K F N W Y V D G V E V H N A

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCA 300

GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTCTGTCATGGCACACCACTCGCAGGAGT

K T K P R E E Q Y N S T Y R V V S V L T

301 CCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360

GGCAGGACGTGGTCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTGTTTC

V L H Q D W L N G K E Y K C K V S N K A

361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420

GGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG

L P A P I E K T I S K A K G Q P R E P Q

421 AGGTGTACACCCTGCCTCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCT 480

TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCCGACTGGA

V Y T L P P S R D E L T K N Q V S L T C

481 GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540

CGGACCAGTTTCCGAAGATAGGGTCTGTAGCGGCACCTCACCTCTCGTTACCCGTCTG

L V K G F Y P S D I A V E W E S N G Q P

541 CGGAGAACAACCTACAAGACACGCTCCCGTCTGGACTCCGACGGCTCCTTCTTCTCTCT 600

GCCTCTTGTGATGTTCTGGTGGGAGGGCAGACCTGAGGCTGCCGAGGAAGAAGGAGA

E N N Y K T T P P V L D S D G S F F L Y

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660

TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCTCCCTTGCAGAAGAGTACGAGGC

S K L T V D K S R W Q Q G N V F S C S V

661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTA 720

ACTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCAT

M H E A L H N H Y T Q K S L S L S P G K

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780

TTCCACCTCCACCACCGCTCCATGAATGAGAACGTTGAAGCCGGGTGACTGAACCAAA

G G G G G G G T Y S C H F G P L T W V C

781 GCAAACCGCAGGTGGCGGCGGCGGCGGCGGTGTTACCTATTCTGTCAATTTTGGCCCGC 840

CGTTTGGCGTCCACCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

K P Q G G G G G G G G T Y S C H F G P L

BamHI

841 TGACCTGGGTATGTAAGCCACAAGGGGTTAATCTCGAGGATCC 884

ACTGGACCCATACATTGGGTGTTCCCCCAATTAGAGCTCCTAGG

T W V C K P Q G G \*



# FIG. 17A

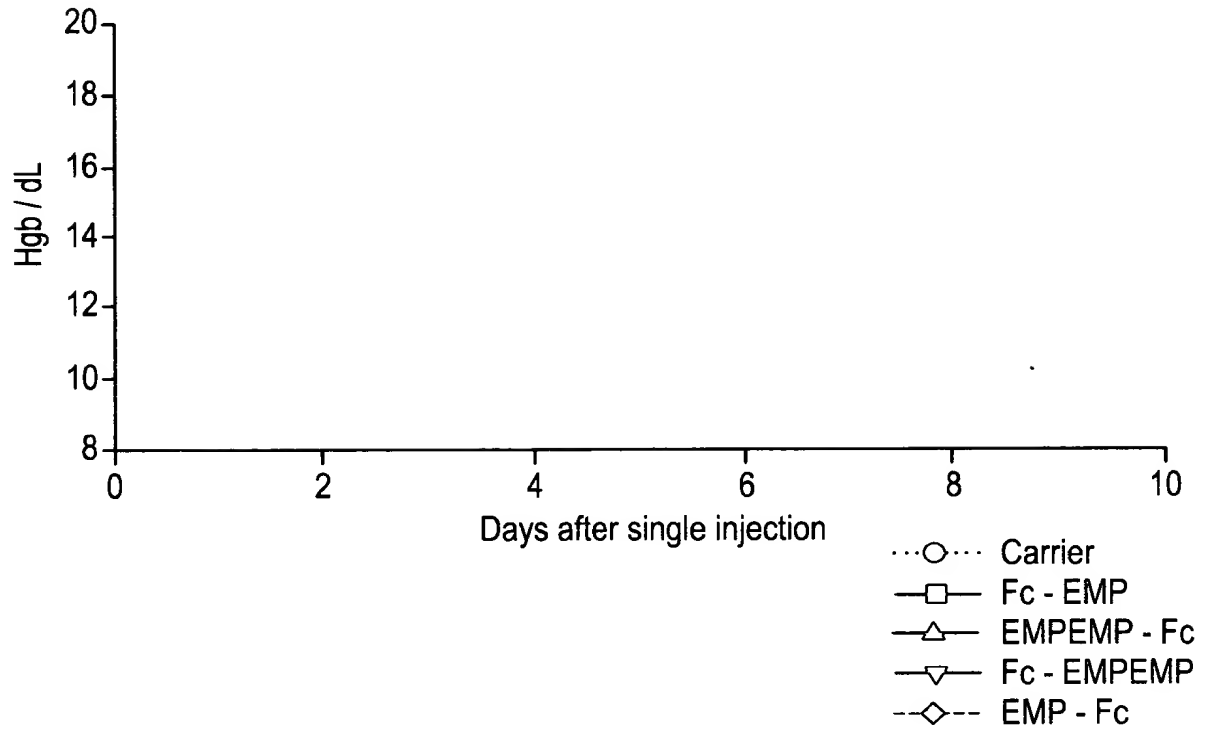
[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-  
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-  
-GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA-  
-GGGCCTTTTCGTTTTATCTGTTGTTTGTCTGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-  
-CCCGGAAAGCAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCTGTTTAGGCG-  
-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG-  
-GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCACCGCCCGTCTGCGGGCG-  
-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCTGACGGATGGCCTTTTTGCGT-  
-GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-  
AatII  
-TTCTACAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-  
-AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-  
-TTTTAAAGTATGGGCAATCAATTGCTCCTGTAAATTTGCTTTAGAAATACTTTGGCAGC-  
-AAAATTTCATACCCGTTAGTTAACGAGGACAATTTAACGAAATCTTTATGAAACCGTCG-  
-GGTTTGTTGTATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC-  
-CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACCTGGCACGCGAATG-  
-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCCACGCTAAAC-  
-ATGTCGGATTATAAAAACTTTATAGGGTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-  
-ATTCTTTTTCTCTTTTGTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTTC-  
-TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAAG-  
-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-  
-CTATTAATAGTTGATCTCTTCTTGTAAATTACCATAACAAGTATGTGCGTACATTTTTAT-  
-AACTATCTATATAGTTGTCTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-  
-TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTGTAAGGCTTCGGTAATA-  
-TAGCAGTATGAATAGGGAACATAACCCAGTGATAAGACCTGATGATTTGCTTCTTTAA-  
-ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-  
-TTACATTTGGAGATTTTTTATTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG-  
-AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC-  
-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-  
-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-  
-AATATTGCCTCCATTTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-  
-TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC-  
-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-  
-TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-  
-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-  
-TATTCGTAACATAATTATAGTAATAACGAAGATGTCCGAAATTAAAAATAATTAATAAGACA-  
-AAGTGTCGTCGGCATTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-  
-TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-  
-GCAAGTTTTGCGTGTTATATATCATTAAACGGTAATAGATTGACATTTGATTCTAATAA-  
-CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

# FIG. 17B

- ATTGGATTTTGTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -  
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTAAACAAATTGTATTCATGGAC -  
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -  
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -  
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -  
- GATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -  
- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -  
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -  
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -  
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -  
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -  
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -  
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]  
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

# FIG.18A - 1



# FIG.18A - 2

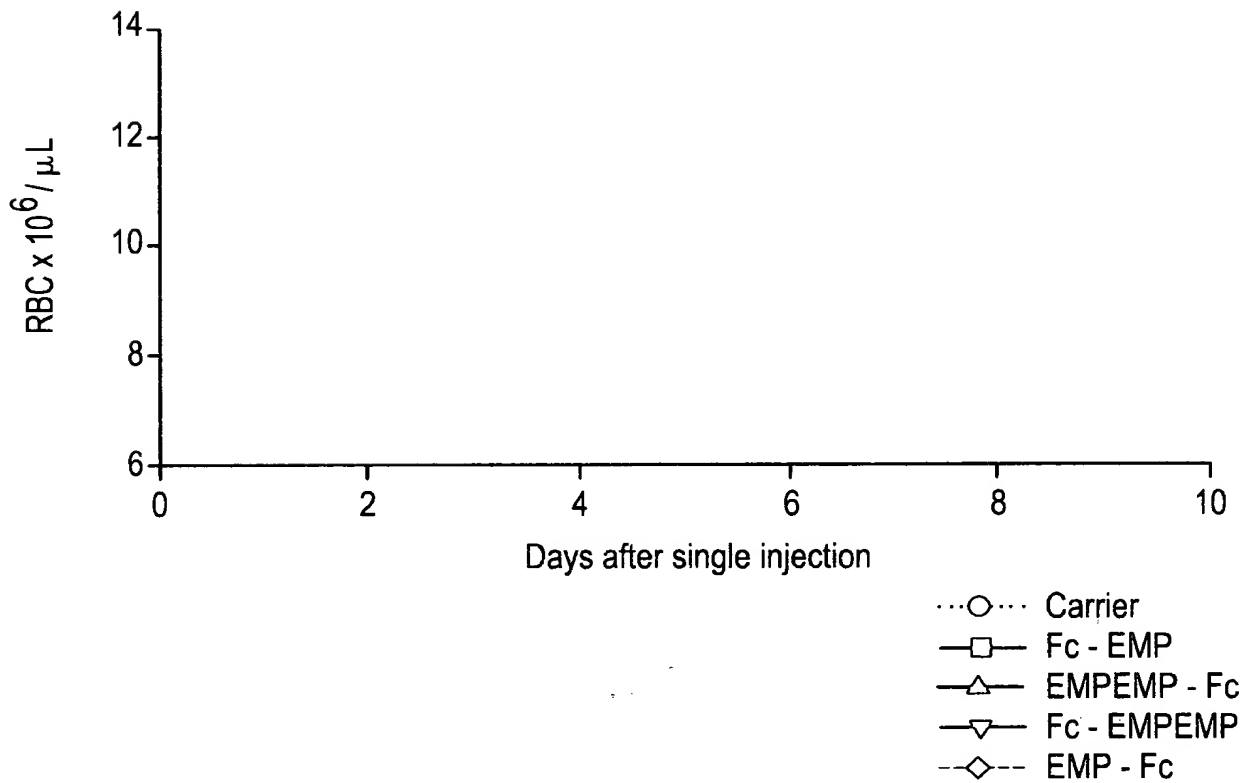


FIG.18A - 3



FIG.18B - 1

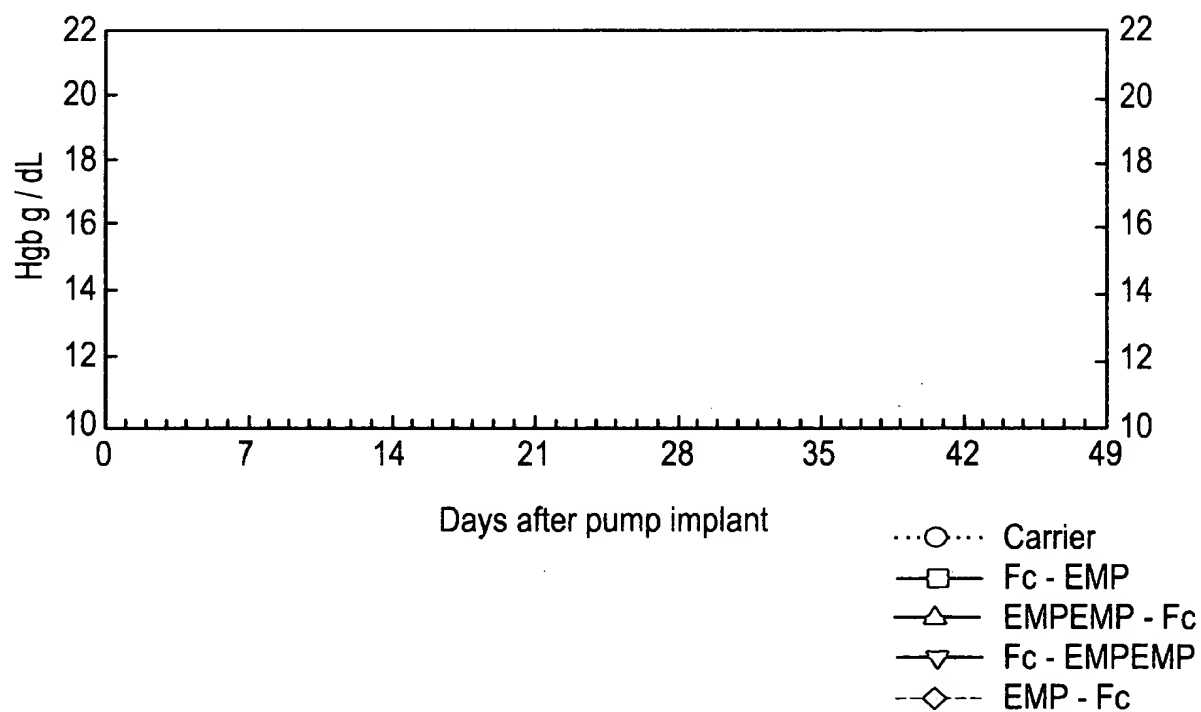


FIG.18B - 2

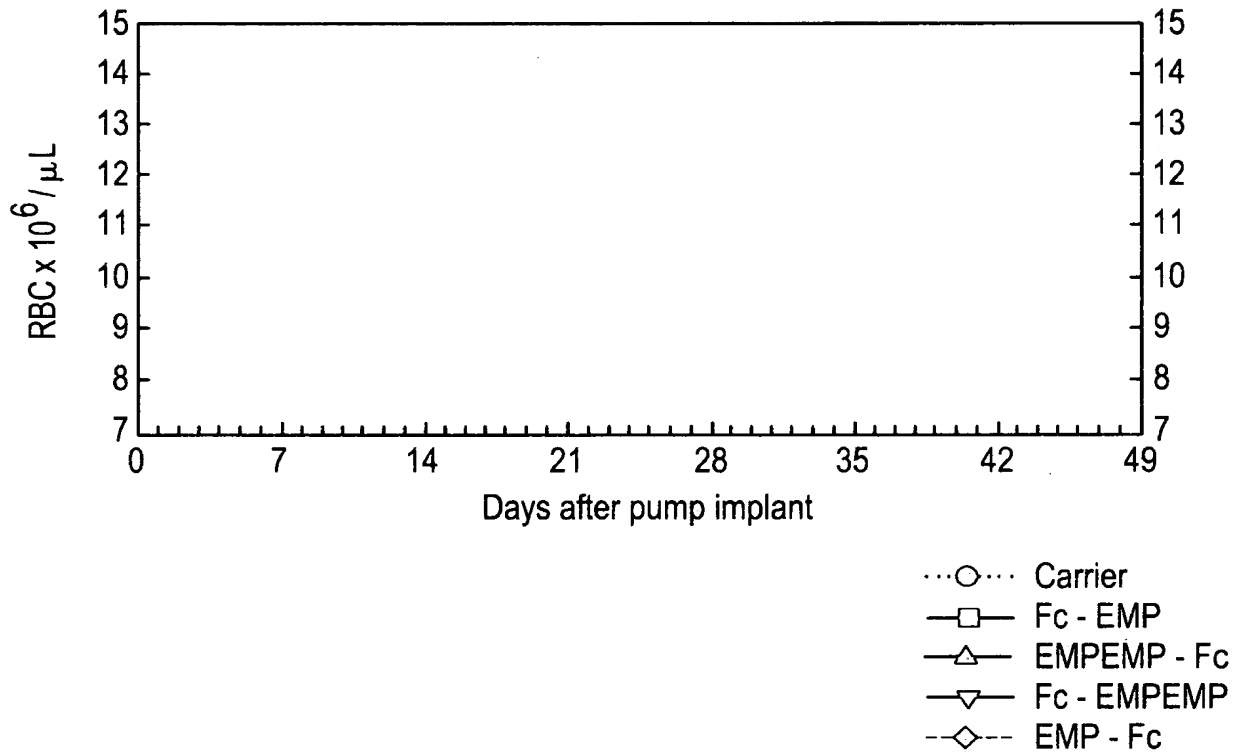
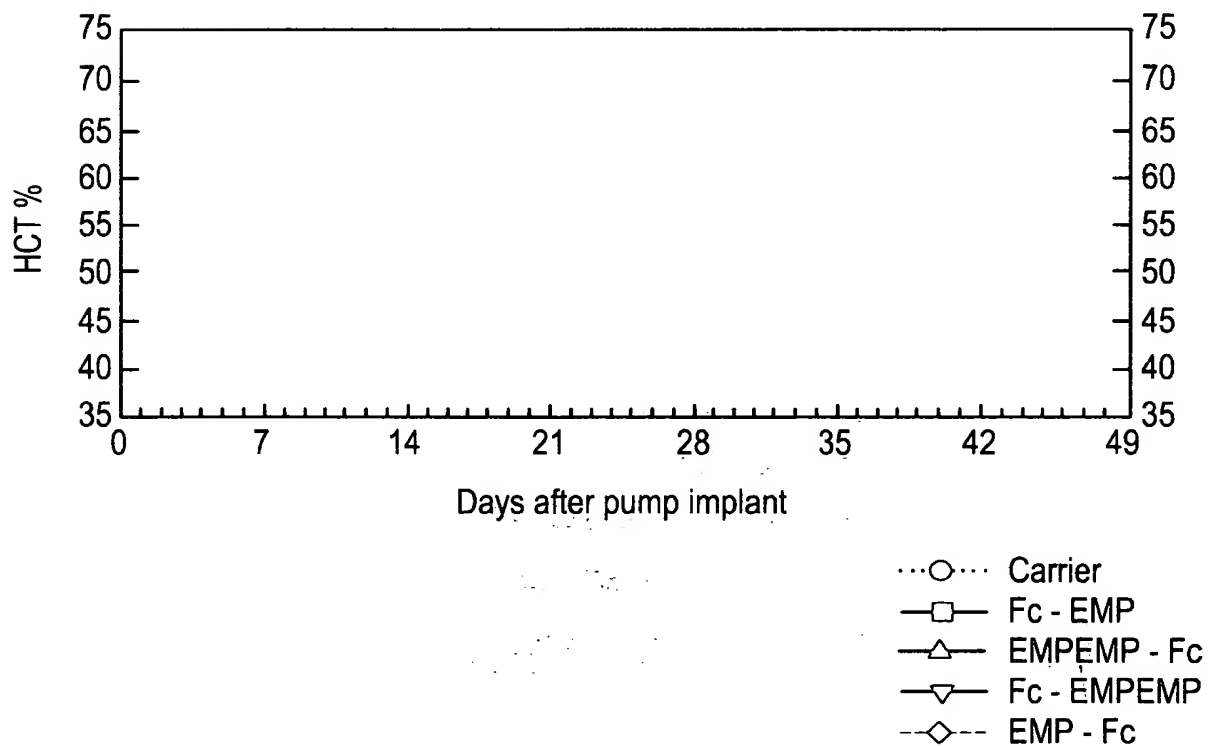


FIG.18B - 3



# FIG. 19A

NdeI

1  
 CATATGGACAAAACTCACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCG  
 -----+-----+-----+-----+-----+-----+-----+ 60  
 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC  
 a M D K T H T C P P C P A P E L L G G P -  
 TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 AGTCAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
 a S V F L F P P K P K D T L M I S R T P E -  
 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
 a V T C V V V D V S H E D P E V K F N W Y -  
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG  
 a V D G V E V H N A K T K P R E E Q Y N S -  
 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
 a T Y R V V S V L T V L H Q D W L N G K E -  
 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
 a Y K C K V S N K A L P A P I E K T I S K -  
 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
 361 -----+-----+-----+-----+-----+-----+-----+ 420  
 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
 a A K G Q P R E P Q V Y T L P P S R D E L -  
 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC  
 421 -----+-----+-----+-----+-----+-----+-----+ 480  
 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
 a T K N Q V S L T C L V K G F Y P S D I A -  
 GTGGAGTGGGAGAGCAATGGGCAGCCGAGACAACACTACAAGACCACGCCTCCCGTGCTG  
 481 -----+-----+-----+-----+-----+-----+-----+ 540  
 CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC  
 a V E W E S N G Q P E N N Y K T T P P V L -  
 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
 541 -----+-----+-----+-----+-----+-----+-----+ 600  
 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC  
 a D S D G S F F L Y S K L T V D K S R W Q -

AF 100-100	FIG.
CLASS	SUBCLASS
DRAFTSMAN	

## FIG. 19B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660  
-----+-----+-----+-----+-----+-----+-----+  
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC 720  
-----+-----+-----+-----+-----+-----+-----+  
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a K S L S L S P G K G G G G G D F L P H Y -

BamHI  
|  
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC 757  
-----+-----+-----+-----+-----+-----+  
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a K N T S L G H R P \*

[illegible]



ATTN	FIG.
CLASS	SUBCLASS
DRAFTSMAN	

# FIG. 20B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a   Q G N V F S C S V M H E A L H N H Y T Q -

BamHI
      |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
-----+-----+-----+-----+-----+ 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC
a   K S L S L S P G K *
```

# FIG. 21A

NdeI  
|

```

1  CATATGGACAAAACCTCACACATGTCCACCTTGTCAGCTCCGGAACCTCCTGGGGGGACCG
   +-----+-----+-----+-----+-----+-----+
a  M D K T H T C P P C P A P E L L G G P -
   TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
61 +-----+-----+-----+-----+-----+-----+ 120
   AGTCAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC
a  S V F L F P P K P K D T L M I S R T P E -
   GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
121 +-----+-----+-----+-----+-----+-----+ 180
   CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG
a  V T C V V V D V S H E D P E V K F N W Y -
   GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
181 +-----+-----+-----+-----+-----+-----+ 240
   CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC
a  V D G V E V H N A K T K P R E E Q Y N S -
   ACGTACCGTGTGGTCAGCGTCCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAG
241 +-----+-----+-----+-----+-----+-----+ 300
   TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC
a  T Y R V V S V L T V L H Q D W L N G K E -
   TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
301 +-----+-----+-----+-----+-----+-----+ 360
   ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT
a  Y K C K V S N K A L P A P I E K T I S K -
   GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
361 +-----+-----+-----+-----+-----+-----+ 420
   CGGTTTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC
a  A K G Q P R E P Q V Y T L P P S R D E L -
   ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC
421 +-----+-----+-----+-----+-----+-----+ 480
   TGGTTCTTGGTCCAGTCGGACTGGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGG
a  T K N Q V S L T C L V K G F Y P S D I A -
   GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
481 +-----+-----+-----+-----+-----+-----+ 540
   CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGCAGGAC
a  V E W E S N G Q P E N N Y K T T P P V L -
   GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
541 +-----+-----+-----+-----+-----+-----+ 600
   CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a  D S D G S F F L Y S K L T V D K S R W Q -

```

APR 1980	7. FIG.
CLASS	SUBCLASS
DRAFTSMAN	

## FIG. 21B

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660  
-----+-----+-----+-----+-----+-----+  
GTCCCCCTTGCAAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC  
a Q G N V F S C S V M H E A L H N H Y T Q -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT 720  
-----+-----+-----+-----+-----+-----+  
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA  
a K S L S L S P G K G G G G G F E W T P G -

BamHI  
|  
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG 763  
-----+-----+-----+-----+-----+  
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC  
a Y W Q P Y A L P L \*

# FIG. 22A

NdeI  
|  
1 CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC 60  
-----+-----+-----+-----+-----+-----+  
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG  
a M F E W T P G Y W Q P Y A L P L G G G -  
61 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 120  
-----+-----+-----+-----+-----+-----+  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
121 TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 180  
-----+-----+-----+-----+-----+-----+  
AGTCAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 240  
-----+-----+-----+-----+-----+-----+  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 300  
-----+-----+-----+-----+-----+-----+  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
301 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 360  
-----+-----+-----+-----+-----+-----+  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA 420  
-----+-----+-----+-----+-----+-----+  
ATGTTACAGTTCCAGAGTTGTTTCGGGAGGGTGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 480  
-----+-----+-----+-----+-----+-----+  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
481 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC 540  
-----+-----+-----+-----+-----+-----+  
TGGTTCCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
541 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCTCCCGTGCTG 600  
-----+-----+-----+-----+-----+-----+  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -

APP.	FIG.
E.	SS SUBCLASS
DRAFTSMAN	

## FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
661 -----+-----+-----+-----+-----+-----+ 720
GTCCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 -----+-----+-----+-----+-----+ 757
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a   K S L S L S P G K *
```

# FIG. 23A

NdeI  
|

```

1  CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG
   -----+-----+-----+-----+-----+-----+-----+
a      M D K T H T C P P C P A P E L L G G P -
61  TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG
   -----+-----+-----+-----+-----+-----+-----+
a      S V F L F P P K P K D T L M I S R T P E -
121 AGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC
   -----+-----+-----+-----+-----+-----+-----+
a      V T C V V V D V S H E D P E V K F N W Y -
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC
   -----+-----+-----+-----+-----+-----+-----+
a      V D G V E V H N A K T K P R E E Q Y N S -
241 ACGTACCGTGTGGTCAGCGTCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAG
   -----+-----+-----+-----+-----+-----+-----+
a      T Y R V V S V L T V L H Q D W L N G K E -
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA
   -----+-----+-----+-----+-----+-----+-----+
a      Y K C K V S N K A L P A P I E K T I S K -
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG
   -----+-----+-----+-----+-----+-----+-----+
a      A K G Q P R E P Q V Y T L P P S R D E L -
421 ACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
   -----+-----+-----+-----+-----+-----+-----+
a      T K N Q V S L T C L V K G F Y P S D I A -
481 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTG
   -----+-----+-----+-----+-----+-----+-----+
a      V E W E S N G Q P E N N Y K T T P P V L -
541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
   -----+-----+-----+-----+-----+-----+-----+
a      D S D G S F F L Y S K L T V D K S R W Q -
600 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

```

# FIG. 23B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG

a   K   S   L   S   L   S   P   G   K   G   G   G   G   G   V   E   P   N   C   D   -

                                     BamHI
                                     |
721 ATCCATGTTATGTGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC
-----+-----+-----+-----+-----+-----+ 773
TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a   I   H   V   M   W   E   W   E   C   F   E   R   L   *

```

# FIG. 24A

NdeI  
|  
CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA

a M V E P N C D I H V M W E W E C F E R -

CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTC  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
GACCCACCACCACCACCACTGTTTTGAGTGTGTACAGGTGGCAGGGTCGTGGACTTGAG

a L G G G G G D K T H T C P P C P A P E L -

CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCC  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGG

a L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG  
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG  
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGAC

a Q Y N S T Y R V V S V L T V L H Q D W L -

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA  
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
TTACCGTTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a N G K E Y K C K V S N K A L P A P I E K -

ACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC  
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a T I S K A K G Q P R E P Q V Y T L P P S -

CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC  
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
GCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGG

a R D E L T K N Q V S L T C L V K G F Y P -

AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG  
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC

a S D I A V E W E S N G Q P E N N Y K T T -



FIG. 24B

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG  
-----+-----+-----+-----+-----+-----+ 660  
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC  
a P P V L D S D G S F F L Y S K L T V D K -  
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC  
661 -----+-----+-----+-----+-----+ 720  
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG  
a S R W Q Q G N V F S C S V M H E A L H N -  
BamHI  
|  
CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC  
721 -----+-----+-----+-----+-----+ 773  
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG  
a H Y T Q K S L S L S P G K \*

FIG. 25A

NdeI  
|  
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
TCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
TGGTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGCTG  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

FIG. 25B		
BY	CLASS	SUBCLASS
RAFTSMAN		

## FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A   K   S   L   S   L   S   P   G   K   G   G   G   G   G   C   T   T   H   W   G   -

          BamHI
          |
721 TTCACCCTGTGCTAATGGATCCCTCGAG
-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a   F   T   L   C   *
```

# FIG. 26A

NdeI  
|

```

1  CATATGTGCACCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT 60
   +-----+-----+-----+-----+-----+-----+
   GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a      M C T T H W G F T L C G G G G G D K G -

61  GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG
   +-----+-----+-----+-----+-----+-----+
   CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGTTGAGGACCC

a      G G G G D K T H T C P P C P A P E L L G -

121 GGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACC
   +-----+-----+-----+-----+-----+-----+
   CCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG

a      G P S V F L F P P K P K D T L M I S R T -

181 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
   +-----+-----+-----+-----+-----+-----+
   GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a      P E V T C V V V D V S H E D P E V K F N -

241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC
   +-----+-----+-----+-----+-----+-----+
   ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a      W Y V D G V E V H N A K T K P R E E Q Y -

301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC
   +-----+-----+-----+-----+-----+-----+
   TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCG

a      N S T Y R V V S V L T V L H Q D W L N G -

361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATC
   +-----+-----+-----+-----+-----+-----+
   TTCCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a      K E Y K C K V S N K A L P A P I E K T I -

421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT
   +-----+-----+-----+-----+-----+-----+
   AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA

a      S K A K G Q P R E P Q V Y T L P P S R D -

481 GAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGAC
   +-----+-----+-----+-----+-----+-----+
   CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG

a      E L T K N Q V S L T C L V K G F Y P S D -

541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCC
   +-----+-----+-----+-----+-----+-----+
   TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC GGAGGG

a      I A V E W E S N G Q P E N N Y K T T P P -

```

APP	FIG.
CLASS	SUBCLASS
DRAFTSMAN	

## FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC

a      V L D S D G S F F L Y S K L T V D K S R -

661 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
-----+-----+-----+-----+-----+-----+ 720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG

a      W Q Q G N V F S C S V M H E A L H N H Y -

                                           BamHI
                                           |
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a      T Q K S L S L S P G K *
```

FIG. 2A

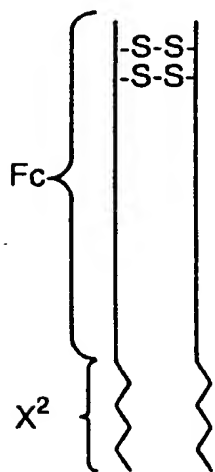


FIG. 2B

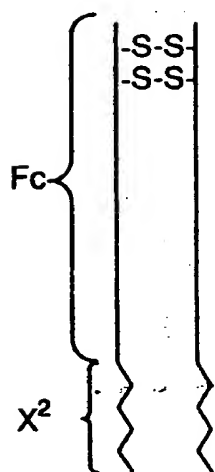


FIG. 2C

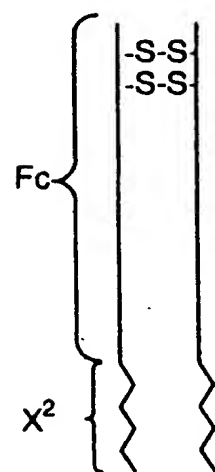


FIG. 2D

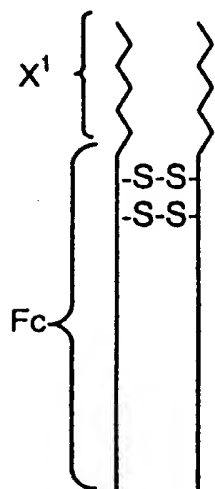


FIG. 2E

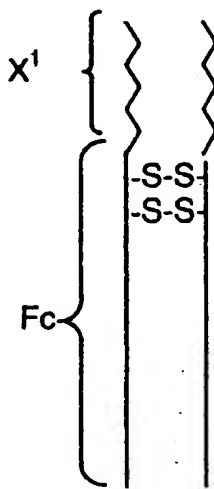


FIG. 2F

